



SEQUENCE LISTING

TRADE
110 Logemann, Juergen
Jach, Guido
Gornhardt, Birgit
Mundy, John
Schell, Jeff
Eckes, Peter
Chet, Ilan

<120> Transgenic pathogen-resistant organism

<130> A29542-FWC-I-R 070037.0195

<140> US 09/729,141

<141> 2000-12-01

<150> 08/812,025

<151> 1997-03-06

<150> 08/457,797

<151> 1995-06-01

<150> 08/134,416

<151> 1993-10-08

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 $\langle 220 \rangle$

<221> CDS

$\langle 222 \rangle \quad (46) \dots (225)$

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aga gcg cgg gtt ttg gcc aca tac aat ggc aaa tgc tac aag aag gat 105
Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp
5 10 15 20

aat atc tgc aag tac aag gca cag agc ggc aag act gcc att tgc aag 153
 Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys
 25 30 35

tgc tat gtc aaa aag tgc ccc cgc gac ggc gcg aaa tgc gag ttt gac 201
 Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp
 40 45 50

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<221> mat_peptide
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 Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala Thr Phe Asn Val
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 Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala Gly Ile Arg Asn
 25 30 35

 aag ctc cgc aac ccg gcg cac ttc tcc cac aac cgc ccc gtg ctg ccg 198
 Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro
 40 45 50

 ccg gtc gag ccc aac gtc ccg ccg agc agg tgg ttc cac gtc gtg ctc 246
 Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu
 55 60 65

 aag gcc tcg ccg acc agc gcc ggg ctc acg ctg gcc att cgg gcg gac 294
 Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp

70				75				80								
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ctc Leu	acc Thr	ccg Pro	ggc Gly 105	ctc Leu 105	atc Ile	ccc Pro	ggc Gly	gcc Ala	acc Thr 110	tac Tyr	gtc Val	ggg Gly	ttc Phe	ggc Gly 115	ggc Gly	390
acc Thr	tac Tyr	cgc Arg	gac Asp 120	ctc Leu	ctc Leu	ggc Gly	gac Asp	acc Thr 125	gac Asp	aag Lys	ctg Leu	acc Thr	aac Asn 130	gtc Val	gct Ala	438
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acc Thr 150	aag Lys	gcc Ala	gac Asp	aag Lys	ccg Pro	tcc Ser 155	ggc Gly	ccg Pro	aag Lys	cag Gln 160	cag Gln	cag Gln	gcg Ala	agg Arg	gag Glu	534
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ccg Pro 230	gga Gly	aag Lys	tcg Ser	cca Pro	gcg Ala	aag Lys 235	ttc Phe	gcg Ala	ccg Pro	atc Ile	gag Glu 240	aag Lys	atg Met	ggc Gly	gtg Val	774
agg Arg 245	acg Thr	gct Ala	gta Val	cag Gln	gcc Ala 250	gcc Ala	aac Asn	acg Thr	ctg Leu	ggg Gly 255	atc Ile	ctg Leu	ctg Leu	ttc Phe	gtg Val 260	822
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 Ala Ser Gly Gly Lys
 280

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 <213> Hordeum vulgare

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 Gly Ile Arg Asn Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg
 35 40 45
 Pro Val Leu Pro Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe
 50 55 60
 His Val Val Leu Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala
 65 70 75 80
 Ile Arg Ala Asp Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly
 85 90 95
 Thr Trp Trp Glu Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val
 100 105 110
 Gly Phe Gly Gly Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu
 115 120 125
 Thr Asn Val Ala Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala
 130 135 140
 Leu His Gly Arg Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln
 145 150 155 160
 Gln Ala Arg Glu Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala
 165 170 175
 Thr Arg Phe Gln Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro
 180 185 190
 Lys Ala Val Glu Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala
 195 200 205
 Gln Val Asn Gly Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp
 210 215 220
 Val Lys Pro Pro Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu
 225 230 235 240
 Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile
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 acg gtg tcg ggg ttc gtg gcc ggg ctg ctg cac ccc aag gcg gtg gag 96
 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu
 20 25 30
 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg 144
 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly
 35 40 45
 tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag ccc ccg 192
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
 50 55 60
 ccg gga aag tcg cca gcg aag ttc acg ccg atc gag aag atg ggc gtg 240
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
 65 70 75 80
 agg act gct gag cag gct gcg gct act ttg ggg atc ctg ctg ttc gtt 288

Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
85 90 95

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttt cat 336
Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
100 105 110

gcg agt ggt ggg aaa taggtagttt tgcaggtata cctgcatggg taaatgtaaa 391
Ala Ser Gly Gly Lys
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<210> 7
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<213> Hordeum vulgare

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35 40 45
Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
50 55 60
Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
65 70 75 80
Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
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Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
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Ala Ser Gly Gly Lys
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<222> (1)...(2329)
<223> ChiS gene from plasmid pLChiS from E.coli A5187

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<213> *Hordeum vulgare*

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<221> mat_peptide

<222> (133)...(861)

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Met Arg Ser Leu Ala Val Val Val Ala Val Val Ala Thr Val Ala
1 5 10 15

atg gcc atc ggc acg gcg cgc ggc agc gtg tcc tcc atc gtc tcg cgc 156
Met Ala Ile Gly Thr Ala Arg Gly Ser Val Ser Ser Ile Val Ser Arg
20 25 30

gca cag ttt gac cgc atg ctt ctg cac cgc aac gac ggc gcc tgc cag 204
Ala Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln
35 40 45

gcc aag ggc ttc tac acc tac gac gcc ttc gtc gcc gcc gca gcc gcc 252
Ala Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala
50 55 60

ttc ccg ggc ttc ggc acc acc ggc agc gcc gac gcc cag aag cgc gag	300
Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu	
65 70 75	
gtg gcc gcc ttc cta gca cag acc tcc cac gag acc acc ggc ggg tgg	348
Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp	
80 85 90 95	
gcg act gca ccg gac ggg gcc ttc gcc tgg ggc tac tgc ttc aag cag	396
Ala Thr Ala Pro Asp Gly Ala Phe Ala Trp Gly Tyr Cys Phe Lys Gln	
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gaa cgt ggc gcc tcc tcc gac tac tgc acc ccg agc gca caa tgg ccg	444
Glu Arg Gly Ala Ser Ser Asp Tyr Cys Thr Pro Ser Ala Gln Trp Pro	
115 120 125	
tgc gcc ccc ggg aag cgc tac tac ggc cgc ggg cca atc cag ctc tcc	492
Cys Ala Pro Gly Lys Arg Tyr Tyr Gly Arg Gly Pro Ile Gln Leu Ser	
130 135 140	
cac aac tac aac tat gga cct gcc ggc cgg gcc atc ggg gtc gat ctg	540
His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val Asp Leu	
145 150 155	
ctg gcc aac ccg gac ctg gtg gcc acg gac gcc act gtg ggc ttt aag	588
Leu Ala Asn Pro Asp Leu Val Ala Thr Asp Ala Thr Val Gly Phe Lys	
160 165 170 175	
acg gcc atc tgg ttc tgg atg acg gcg cag ccg ccc aag cca tcg agc	636
Thr Ala Ile Trp Phe Trp Met Thr Ala Gln Pro Pro Lys Pro Ser Ser	
180 185 190	
cat gct gtg atc gcc ggc cag tgg agc ccg tca ggg gct gac cgg gcc	684
His Ala Val Ile Ala Gly Gln Trp Ser Pro Ser Gly Ala Asp Arg Ala	
195 200 205	
gca ggc cgg gtg ccc ggg ttt ggt gtg atc acc aac atc atc aac ggc	732
Ala Gly Arg Val Pro Gly Phe Gly Val Ile Thr Asn Ile Ile Asn Gly	
210 215 220	
ggg atc gag tgc ggt cac ggg cag gac agc cgc gtc gcc gat cga atc	780
Gly Ile Glu Cys Gly His Gly Gln Asp Ser Arg Val Ala Asp Arg Ile	
225 230 235	
ggg ttt tac aag cgc tac tgt gac atc ctc ggc gtt ggc tac ggc aac	828
Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Leu Gly Val Gly Tyr Gly Asn	

255

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<213> Hordeum vulgare
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Gln	Phe	Asp	Arg	Met	Leu	Leu	His	Arg	Asn	Asp	Gly	Ala	Cys	Gln	Ala
Lys	Gly	Phe	Tyr	Thr	Tyr	Asp	Ala	Phe	Val	Ala	Ala	Ala	Ala	Ala	Phe
Pro 65	Gly	Phe	Gly	Thr	Thr	Gly	Ser	Ala	Asp	Ala	Gln	Lys	Arg	Glu	Val 80
Ala	Ala	Phe	Leu	Ala	Gln	Thr	Ser	His	Glu	Thr	Thr	Gly	Gly	Trp	Ala
Thr	Ala	Pro	Asp	Gly	Ala	Phe	Ala	Trp	Gly	Tyr	Cys	Phe	Lys	Gln	Glu
Arg	Gly	Ala	Ser	Ser	Asp	Tyr	Cys	Thr	Pro	Ser	Ala	Gln	Trp	Pro	Cys
Ala	Pro	Gly	Lys	Arg	Tyr	Tyr	Gly	Arg	Gly	Pro	Ile	Gln	Leu	Ser	His
Asn 145	Tyr	Asn	Tyr	Gly	Pro	Ala	Gly	Arg	Ala	Ile	Gly	Val	Asp	Leu	Leu 160
Ala	Asn	Pro	Asp	Leu	Val	Ala	Thr	Asp	Ala	Thr	Val	Gly	Phe	Lys	Thr
Ala	Ile	Trp	Phe	Trp	Met	Thr	Ala	Gln	Pro	Pro	Lys	Pro	Ser	Ser	His
Ala	Val	Ile	Ala	Gly	Gln	Trp	Ser	Pro	Ser	Gly	Ala	Asp	Arg	Ala	Ala
Gly	Arg	Val	Pro	Gly	Phe	Gly	Val	Ile	Thr	Asn	Ile	Ile	Asn	Gly	Gly
Ile 225	Glu	Cys	Gly	His	Gly	Gln	Asp	Ser	Arg	Val	Ala	Asp	Arg	Ile	Gly 240
Phe	Tyr	Lys	Arg	Tyr	Cys	Asp	Ile	Leu	Gly	Val	Gly	Tyr	Gly	Asn	Asn
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<210> 11
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<220>
 <221> 5'UTR
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<221> polyA_signal
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<221> mat_peptide
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 Met Ala Arg
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 Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe
 5 10 15

gct gct gtt cct acg agt gtg cag tcc atc ggc gta tgc tac ggc gtg 153
 Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val
 20 25 30 35

atc ggc aac aac ctc ccc tcc cgg agc gac gtg gtg cag ctc tac agg 201
 Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg
 40 45 50

tcc aag ggc atc aac ggc atg cgc atc tac ttc gcc gac ggg cag gcc 249
 Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala
 55 60 65

ctc tgc gcc gtc cgc aac tcc gcc atc gcc ctc atc ctc gac atc gcc 297
 Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu Asp Ile Gly
 70 75 80

aac gac cag ctc gcc aac atc gcc gcc agc acc tcc aac gcg gcc tcc 345
 Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn Ala Ala Ser
 85 90 95

tgg gtc cag aac aac gtg cgg ccc tac tac cct gcc gtg aac atc aag 393
 Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val Asn Ile Lys
 100 105 110 115

tac atc gcc gcc gcc aac gag gtg cag gcc gcc gcc acg cag agc atc 441
 Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr Gln Ser Ile
 120 125 130

ctg ccg gcc atg cgc aac ctc aac gcg gcc ctc tcc gcg gcg ggg ctc 489
 Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala Ala Gly Leu
 135 140 145

gcc gcc atc aag gtg tcc acc tcc atc cgg ttc gac gag gtg gcc aac 537
 Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu Val Ala Asn
 150 155 160

tcc ttc ccg ccc tcc gcc gcc gtg ttc aag aac gcc tac atg acg gac 585
 Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr Met Thr Asp
 165 170 175

gtg gcc ccg ctc ctg gcg agc acc gcc gcg ccg ctg ctc gcc aac gtc 633
 Val Ala Arg Leu Leu Ala Ser Thr Gly Ala Pro Leu Leu Ala Asn Val
 180 185 190 195

tac ccc tac ttc gcg tac cgt gac aac ccc ggg agc atc agc ctg aac 681
 Tyr Pro Tyr Phe Ala Tyr Arg Asp Asn Pro Gly Ser Ile Ser Leu Asn
 200 205 210

tac gcg acg ttc cag ccg gcc acc acc gtg cgt gac cag aac aac ggg 729
 Tyr Ala Thr Phe Gln Pro Gly Thr Thr Val Arg Asp Gln Asn Asn Gly
 215 220 225

ctg acc tac acg tcc ctg ttc gac gcg atg gtg gac gcc gtg tac gcg 777
 Leu Thr Tyr Thr Ser Leu Phe Asp Ala Met Val Asp Ala Val Tyr Ala
 230 235 240

gcg ctg gag aag gcc gcc gcg ccg gcg gtg aag gtg gtg gtg tcg gag 825
 Ala Leu Glu Lys Ala Gly Ala Pro Ala Val Lys Val Val Val Ser Glu
 245 250 255

agc ggg tgg ccg tcg gcg gcc ggg ttt gcg gcg tcg gcc gcc aat gcg 873

Ser Gly Trp Pro Ser Ala Gly Gly Phe Ala Ala Ser Ala Gly Asn Ala
260 265 270 275

cgg acg tac aac cag ggg ctg atc aac cac gtc ggc ggg ggc acg ccc 921
Arg Thr Tyr Asn Gln Gly Leu Ile Asn His Val Gly Gly Gly Thr Pro
280 285 290

aag aag cgg gag gcg ctg gag acg tac atc ttc gcc atg ttc aac gag 969
Lys Lys Arg Glu Ala Leu Glu Thr Tyr Ile Phe Ala Met Phe Asn Glu
295 300 305

aac cag aag acc ggg gac gcc acg gag agg agc ttc ggg ctc ttc aac 1017
Asn Gln Lys Thr Gly Asp Ala Thr Glu Arg Ser Phe Gly Leu Phe Asn
310 315 320

ccg gac aag tcg ccg gca tac aac atc cag ttc tagtacgtgt agctacctag 1070
Pro Asp Lys Ser Pro Ala Tyr Asn Ile Gln Phe
325 330

ctcacataacc taaataaata agctgcacgt acgtacgtaa tgcggcatcc aagtgtaacg 1130
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<211> 334

<212> PRT

<213> Hordeum vulgare

<400> 12

Met Ala Arg Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile
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Gly Ala Phe Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys
20 25 30
Tyr Gly Val Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln
35 40 45
Leu Tyr Arg Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp
50 55 60
Gly Gln Ala Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu
65 70 75 80
Asp Ile Gly Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn
85 90 95
Ala Ala Ser Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val
100 105 110
Asn Ile Lys Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Ala Thr
115 120 125
Gln Ser Ile Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala
130 135 140
Ala Gly Leu Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu
145 150 155 160
Val Ala Asn Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr

Met	Thr	Asp	Val	165 Ala	Arg	Leu	Leu	Ala	170 Ser	Thr	Gly	Ala	Pro	175 Leu	Leu
Ala	Asn	Val	180 Tyr	Pro	Tyr	Phe	Ala	185 Tyr	Arg	Asp	Asn	Pro	190 Gly	Ser	Ile
Ser	Leu	Asn	195 Tyr	Ala	Thr	Phe	Gln	200 Pro	Gly	Thr	Thr	Val	Arg	Asp	Gln
Asn	Asn	Gly	Leu	Thr	Tyr	Thr	Ser	Leu	Phe	Asp	Ala	Met	Val	Asp	Ala
225	Val	Tyr	Ala	Ala	Leu	Glu	Lys	Ala	Gly	Ala	Pro	Ala	Val	Lys	Val
Val	Ser	Glu	Ser	Gly	Trp	Pro	Ser	Ala	Gly	Gly	Phe	Ala	Ala	Ser	Ala
Gly	Asn	Ala	Arg	Thr	Tyr	Asn	Gln	Gly	Leu	Ile	Asn	His	Val	Gly	Gly
Gly	Thr	Pro	Lys	Lys	Arg	Glu	Ala	Leu	Glu	Thr	Tyr	Ile	Phe	Ala	Met
Phe	Asn	Glu	Asn	Gln	Lys	Thr	Gly	Asp	Ala	Thr	Glu	Arg	Ser	Phe	Gly
305	Leu	Phe	Asn	Pro	Asp	Lys	Ser	Pro	Ala	Tyr	Asn	Ile	Gln	Phe	
				325					330						